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Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search for

Limits

Preview/Index

History

Clipboard

Details

Show: ☐ 1: [NM_006044](#). Homo sapiens hist...[gi:13128863]

Links

LOCUS NM_006044 4099 bp mRNA linear PRI 04-OCT-2003

DEFINITION Homo sapiens histone deacetylase 6 (HDAC6), mRNA.

ACCESSION NM_006044

VERSION NM_006044.2 GI:13128863

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4099)

AUTHORS Hook,S.S., Orian,A., Cowley,S.M. and Eisenman,R.N.

TITLE Histone deacetylase 6 binds polyubiquitin through its zinc finger (PAZ domain) and copurifies with deubiquitinating enzymes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (21), 13425-13430 (2002)

MEDLINE 22269913

PUBMED 12354939

REMARK GeneRIF: the C terminus of HDAC 6 is both necessary and sufficient for specific association with polyubiquitin

REFERENCE 2 (bases 1 to 4099)

AUTHORS Mahlknecht,U., Schnittger,S., Landgraf,F., Schoch,C., Ottmann,O.G., Hiddemann,W. and Hoelzer,D.

TITLE Assignment of the human histone deacetylase 6 gene (HDAC6) to X chromosome p11.23 by in situ hybridization

JOURNAL Cytogenet. Cell Genet. 93 (1-2), 135-136 (2001)

MEDLINE 21367618

PUBMED 11474198

REFERENCE 3 (bases 1 to 4099)

AUTHORS Grozinger,C.M., Hassig,C.A. and Schreiber,S.L.

TITLE Three proteins define a class of human histone deacetylases related to yeast Hda1p

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (9), 4868-4873 (1999)

MEDLINE 99238449

PUBMED 10220385

REFERENCE 4 (bases 1 to 4099)

AUTHORS Pazin,M.J. and Kadonaga,J.T.

TITLE What's up and down with histone deacetylation and transcription?

JOURNAL Cell 89 (3), 325-328 (1997)

MEDLINE 97294375

PUBMED 9150131

REFERENCE 5 (bases 1 to 4099)

AUTHORS Wolffe,A.P.

TITLE Transcriptional control. Sinful repression

JOURNAL Nature 387 (6628), 16-17 (1997)

MEDLINE 97284401

PUBMED 9139815

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [AJ011972.1](#).



On Feb 26, 2001 this sequence version replaced gi:5174488.

Summary: Histones play a critical role in transcriptional regulation, cell cycle progression, and developmental events. Histone acetylation/deacetylation alters chromosome structure and affects transcription factor access to DNA. The protein encoded by this gene belongs to class II of the histone deacetylase/acuc/apha family. It contains an internal duplication of two catalytic domains which appear to function independently of each other. This protein possesses histone deacetylase activity and represses transcription.

COMPLETENESS: complete on the 3' end.

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Oct 28 2003 13:06:52



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

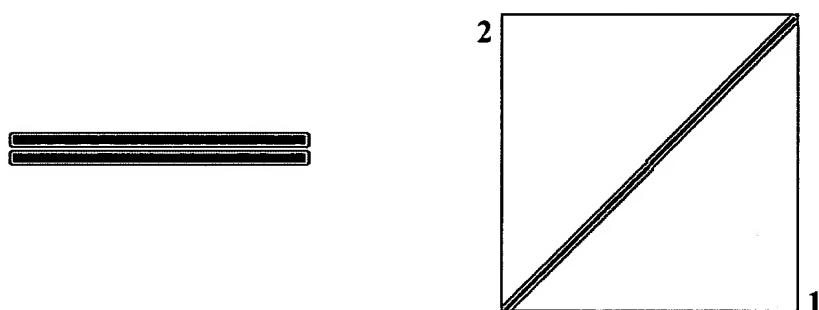
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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Oct-19-2000]

Match: Mismatch: gap open: gap extension:
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Sequence 1 gi 3776070 Homo sapiens mRNA for histone deacetylase-like protein (JM21) **Length** 4099 (1 .. 4099)

Sequence 2 gi 13128863 Homo sapiens histone deacetylase 6 (HDAC6), mRNA **Length** 4099 (1 .. 4099)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

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Query: 1681 cctgccacagaggctgagctgtcacctgtcacagtgtgagtacgtgggtcatctc
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Sbjct: 1681 cctgccacagaggctgagctgtcacctgtcacagtgtgagtacgtgggtcatctc
histone deacetylase 6 530 P A T E A E L L T C H S A E Y V G H L

Query: 1741 gccacagagaaaatgaaaacccgggagctgcaccgtgagagttccaactttgactcc
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histone deacetylase 6 550 A T E K M K T R E L H R E S S N F D S

Query: 1801 tataatctgccccagtaccttcgcctgtgcacagcttgccactggcgctgcctgccgc
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Sbjct: 1801 tataatctgccccagtaccttcgcctgtgcacagcttgccactggcgctgcctgccgc
histone deacetylase 6 570 Y I C P S T F A C A Q L A T G A A C R

Query: 1861 gtggaggctgtgctctcaggagaggttctgaatggtgctgctgtggtgctgccccca
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Query: 1921 caccacgcagagcaggatgcagcttgccggtttttgctttttcaactctgtggctgtg
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Query: 1981 gctcgccatgccagactatcagtgggcatgccctacggatcctgattgtggattgg
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Query: 2041 gtccaccacggtaatggaactcagcacatgtttgaggatgacccagtgctatat
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histone deacetylase 6 650 V H H G N G T Q H M F E D D P S V L Y

Query: 2101 tccctgcaccgctatgatcatggcaccttcttcccatgggggatgagggcgccagc
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histone deacetylase 6 690 Q I G R A A G T G F T V N V A W N G P

Query: 2221 atgggtgatgctgactacctagctgcctggcatcgctggtgcttccattgcctac
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Sbjct: 2221 atgggtgatgctgactacctagctgcctggcatcgctggtgcttccattgcctac
histone deacetylase 6 710 M G D A D Y L A A W H R L V L P I A Y

Query: 2281 tttaaccagaactggtgctggtctcagctggctttgatgctgcacgggggatccg
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Query: 2341 gggggctgccaggtgtcacctgagggttatgccacctcaccacctgctgatgggc
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Query: 2401 gccagtggccgcattatccttatcctagaggggtggctataacctgacatccatctca
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Sbjct: 2401 gccagtggccgcattatccttatcctagaggggtggctataacctgacatccatctca
histone deacetylase 6 770 A S G R I I L I L E G G Y N L T S I S

Query: 2461 tccatggctgcctgcactcgctccctccttggagaccaccaccctgctgaccctg
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Query: 2521 cggccccactatcaggggccctggcctcaatcactgagaccatccaagtccatcgc
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histone deacetylase 6 830 Y W R S L R V M K V E D R E G P S S S

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histone deacetylase 6 850 L V T K K A P Q P A K P R L A E R M T

Query: 2701 cgagaaaagaaggttctggaagcaggcatggggaaagtcacctcggcatcatttggg
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histone deacetylase 6 870 R E K K V L E A G M G K V T S A S F G

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histone deacetylase 6 890 E S T P G Q T N S E T A V V A L T Q D

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Query: 3121 gaggaggctccagggggcaccgagctgatccaaactcctctagcctcgagcacagac
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Query: 3181 cagannnnnnnaacctcacctgtgcagggaactacaccccagatatctcccagtaca
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histone deacetylase 6 1170 H P L V L S Y I D L S A W C Y Y C Q A

Query: 3661 gtccaccaccaggctctcctagatgtgaagaacatcgcccaccagaacaagtttggg
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histone deacetylase 6 1190 V H H Q A L L D V K N I A H Q N K F G

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Sbjct: 3721 gatatgccccacccacactaagccccagaatacgggtccctcttcaccttctgaggcc
histone deacetylase 6 1210 D M P H P H ^^^

Query: 3781 gatagaccagctgtagctcattccagcctgtaccttggatgaggggtagcctccac
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Sbjct: 3781 gatagaccagctgtagctcattccagcctgtaccttggatgaggggtagcctccac

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Sbjct:          3901 taagagaactgcgacgattaattgtggatctccccctgccattgcctgcttgaggg

Query:          3961 ccactactccagcccagaaggaaaggggggcagctcagtggccccaagagggagctg
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Sbjct:          3961 ccactactccagcccagaaggaaaggggggcagctcagtggccccaagagggagctg

Query:          4021 tcatgaggataacattggcgggaggggagttaactggcaggcatggcaaggttgcatt
                |||
Sbjct:          4021 tcatgaggataacattggcgggaggggagttaactggcaggcatggcaaggttgcatt

Query:          4081 taataaagtacaagctggt 4099
                |||
Sbjct:          4081 taataaagtacaagctggt 4099

```

CPU time: 0.21 user secs. 0.09 sys. secs 0.30 total secs.

Gapped
 Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 37
 Number of Sequences: 0
 Number of extensions: 37
 Number of successful extensions: 25
 Number of sequences better than 10.0: 1
 length of query: 4099
 length of database: 4,430,590,239
 effective HSP length: 26
 effective length of query: 4073
 effective length of database: 4,429,730,003
 effective search space: 18042290302219
 effective search space used: 18042290302219
 T: 0
 A: 0
 X1: 6 (11.5 bits)
 X2: 26 (50.0 bits)
 S1: 12 (23.8 bits)
 S2: 21 (41.1 bits)